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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=11; hr=17; min=28; sec=25; ms=669;]

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Validated By CRFValidator v 1.0.3

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<110> YOKOTA, Akiho
SHIGEOKA, Shigeru
TOMIZAWA, Ken-ichi

<120> METHOD FOR IMPROVING PRODUCTIVITY OF PLANT BY CHLOROPLAST TECHNOLOGY

<130> 2006_1303A

<140> 10591752
<141> 2008-07-09

<150> PCT/JP2005/004037
<151> 2005-03-02

<150> JP 2004-059513
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<160> 18

<170> PatentIn version 3.4

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<212> PRT
<213> Spinacia oleracea L

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<223> Fructose-1,6-bisphosphatase

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Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met
20 25 30

Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser
35 40 45

Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser
50 55 60

Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln
65 70 75 80

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Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg
                85                  90                  95

Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro
            100                 105                 110

Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp
        115                 120                 125

Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser
    130                 135                 140

Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp
145                 150                 155                 160

His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val
                165                 170                 175

Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met
            180                 185                 190

Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr
        195                 200                 205

Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu
    210                 215                 220

Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly
225                 230                 235                 240

Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu
                245                 250                 255

Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly
            260                 265                 270

Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr
        275                 280                 285

Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu
    290                 295                 300

Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys
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305 310 315 320

Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile
325 330 335

His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys
340 345 350

Leu Glu Lys Tyr Leu Ala
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<210> 2
<211> 1074
<212> DNA
<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

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gaaacactaa caggctggct gcttaaacaa gaaatggcag gtgttattga tgctgaactt 120

accatcgttc tttctagcat ttcattggct tgtaaacaaa ttgcttcctt ggttcaacga 180

gctggtattt ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag 240

aagaaacttg atgttgtctc caatgaggtg ttttcgagct gcttgagatc gagtggaaga 300

acaggaataa tagcatcaga agaagaggat gtaccagtgg cagtggaaga gagttactct 360

ggaaactata ttgttgtgtt tgatccactt gatggttcat ccaacattga tgcagctgtc 420

tccactggtt ccatctttgg catttatagc cctaacgatg agtgcattgt tgactctgat 480

cacgacgatg agtcacagct aagtgcagaa gaacagaggt gtgtagtgaa tgtatgtcaa 540

ccaggggata acctattagc agcagggtat tgtatgtact caagctctgt tatcttcgta 600

cttacaattg gtaaaggtgt gtatgcattc acattagatc caatgtatgg tgaattcgta 660

ctcacttcag agaaaatcca aatcccaaaa gctgggaaga tctattcatt caatgaaggt 720

aactacaaaa tgtgggatga taaattgaag aagtacatgg atgatcttaa agagccagga 780

gagtcacaga aaccgtactc gtctcgttac atagggagtt tagttgggga ctttcataga 840

acacttttat atggtgggat ttatggttac ccaagagatg caaagagtaa gaatgggaaa 900

ttgaggcttt tgtatgaatg tgcacctatg agttttattg ttgaacaagc tggtggtaaa 960

ggttctgatg gtcatcaaag aattcttgac attcaaccca ccgagataca tcaacgtgtg 1020

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<211> 333
<212> PRT
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1, 7-bisphosphatase

<400> 3

Val Asn Lys Ala Lys Asn Ser Ser Leu Val Thr Lys Cys Glu Leu Gly
1 5 10 15

Asp Ser Leu Glu Glu Phe Leu Ala Lys Ala Thr Thr Asp Lys Gly Leu
20 25 30

Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe
35 40 45

Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe
50 55 60

Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe
65 70 75 80

Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu
85 90 95

Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser
100 105 110

Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe
115 120 125

Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly
130 135 140

Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro
145 150 155 160

Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu
165 170 175

Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr
180 185 190

Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr
195 200 205

Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu
210 215 220

Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln
225 230 235 240

Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr
245 250 255

Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe
260 265 270

Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val
275 280 285

Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr
290 295 300

Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser
305 310 315 320

Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala
325 330

<210> 4
<211> 999
<212> DNA
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1,7-bisphosphatase

<400> 4
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gagttcctag caaaggcaac cacagataaa gggctgatta gattgatgat gtgcatggga 120

gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggtgg aactcaatgt 180

gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc 240

gaggcattga actattcaca cttctgcaag tatgcttgtt cagaagaact ccctgagctt 300

caagatatgg gaggccccgt tgatggcgga ttcagtgtag catttgaccc ccttgatgga 360

tccagcattg tcgataccaa tttctcagtt gggaccatat tcggggtttg gccaggtgac 420

aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggtcct 480

aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttcttctt 540

gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc 600

tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac 660

tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgttaaccag 720

atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag 780

ttgaggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tggtggtcac 840

agcagtgagg gaaccaagtc tgtgttggac attgaagtca aaaaccttga tgacagaacc 900

caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc 960

tctaggctag aggagccagt tcctgttgga gctgctgct 999

<210> 5
<211> 356
<212> PRT
<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus PCC 7942

<400> 5

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1 5 10 15

Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala
20 25 30

Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
35 40 45

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Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
    50                  55                  60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
65                  70                  75                  80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
                85                  90                  95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
            100                 105                 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
        115                 120                 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
    130                 135                 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
145                 150                 155                 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Met Asp Arg
                165                 170                 175

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
            180                 185                 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
        195                 200                 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
    210                 215                 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
225                 230                 235                 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
                245                 250                 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile
            260                 265                 270
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Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln
275 280 285

Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu
290 295 300

Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile
305 310 315 320

Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe
325 330 335

Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp
340 345 350

Arg Pro Glu Arg
355

<210> 6
<211> 1312
<212> DNA
<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus PCC 7942

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gaatccccag aagcaatcat ccgtaaggag tcaggacggc gtggagaaga cgatcggtct 120

cgagattatt gaagttgtcg agcaggcagc gatcgcctcg gcccgcctga tgggcaaagg 180

cgaaaagaat gaagccgatc gcgtcgcagt agaagcgatg cgggtgcgga tgaaccaagt 240

ggaaatgctg ggccgcatcg tcatcggtga aggcgagcgc gacgaagcac cgatgctcta 300

tatcggtgaa gaagtgggca tctaccgcga tgcagacaag cgggctggcg taccggctgg 360

caagctggtg gaaatcgaca tcgccgttga cccctgcgaa ggcaccaacc tctgcgccta 420

cggtcagccc ggctcgatgg cagttttggc catctccgag aaaggcggcc tgtttgcagc 480

tcccgacttc tacatgaaga aactggctgc acccccagct gccaaaggca aagagacatc 540

aataaagtcc gcgaccgaaa acctgaaaat tctctcggaa tgtctcgatc gcgccatcga 600

tgaattggtg gtcgtggtca tggatcgtcc ccgccacaaa gagctaatcc aagagatccg 660

ccaagcgggt gcccgcgtcc gtctgatcag cgatggtgac gtttcggccg cgatctcctg 720

cggttttgct ggcaccaaca cccacgccct gatgggcatc ggtgcagctc ccgagggtgt 780

gatttcggca gcagcaatgc gttgcctcgg cgggcacttc caaggccagc tgatctacga 840

cccagaagtg gtcaaaaccg gcctgatcgg tgaaagccgt gagagcaaca tcgctcgcct 900

gcaagaaatg ggcatcaccg atcccgatcg tgtctacgac gcgaacgaac tggcttcggg 960

tcaagaagtg ctgtttgcgg cttgcggtat caccccgggc ttgctgatgg aaggcgtgcg 1020

cttcttcaaa ggcggcgctc gcacccagag cttggtgatc tccagccagt cacggacggc 1080

tcgcttcgtt gacaccgttc acatgttcga cgatgtcaaa acggttagcc tgccgttaat 1140

tcctgatccc aaatggcggc cggagcggta gaacgggtat agctcgatcg cttcggtcgt 1200

tgtttttcag cgaatccatt tgcgatcgct tttcaaaccc ttttttcgtc aaccttcttt 1260

aaacggcctc atgcatctcg cagttgtcgg ctcagccatc ggacagcacc gg 1312

<210> 7
<211> 133
<212> DNA
<213> Nicotiana tabacum

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<223> psbA promoter

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aagccttcca ttttctattt tgatttgtag aaaactagtg tgcttgggag tccctgatga 120

ttaaataaac caa 133

<210> 8
<211> 159
<212> DNA
<213> Nicotiana tabacum

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<223> rps16 terminator

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tatataactt tgtatgactt ttctcttcta ttttttgta tttcctccct ttccttttct 120

atttgtattt ttttatcatt gcttccattg aattactag 159

<210> 9
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<213> Escherichia coli

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<223> aadA

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gcgtcatcga gcgccatctc gaaccgacgt tgctggccgt acatttgtac ggctccgcag 120

tggatggcgg cctgaagcca cacagtgata ttgatttgct ggttacggtg accgtaaggc 180

ttgatgaaac aacgcggcga gctttgatca acgacctttt ggaaacttcg gcttcccctg 240

gagagagcga gattctccgc gctgtagaag tcaccattgt tgtgcacgac gacatcattc 300

cgtggcgtta tccagctaag cgcgaactgc aatttggaga atggcagcgc aatgacattc 360

ttgcaggtat cttcgagcca gccacgatcg acattgatct ggctatcttg ctgacaaaag 420

caagagaaca tagcgttgcc ttggtaggtc cagcggcgga ggaactcttt gatccggttc 480

ctgaacagga tctatttgag gcgctaaatg aaaccttaac gctatggaac tcgccgcccg 540

actgggctgg cgatgagcga aatgtagtgc ttacgttgtc ccgcatttgg tacagcgcag 600

taaccggcaa aatcgcgccg aaggatgtcg ctgccgactg ggcaatggag cgcctgccgg 660

cccagtatca gcccgtcata cttgaagcta gacaggctta tcttggacaa gaagaagatc 720

gcttggcctc gcgcgcagat cagttggaag aatttgtcca ctacgtgaaa ggcgagatca 780

ctaaggtagt tggcaaataa ctgca 805

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<213> Artificial sequence

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<223> synthetic construct

<220>
<223> pLD6

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caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa 120

ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt 180

gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt 240

tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt 300

ttcgccccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg 360

tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga 420

atgacttggt tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa 480

gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga 540

caacgatcgg aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa 600

ctcgccttga tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca 660

ccacgatgcc tgtagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta 720

ctctagcttc ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac 780

ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc 840

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